

Risultati

*Computational analysis of biological structures and networks*

**Workshop on “Dissimilarity-based approaches in bioinformatics”**

Results July 2017

Measure of synonymous codon usage diversity among genes in bacteria	14/15
New developments of alignment-free sequence comparison: measures, statistics and next-generation sequencing	13.5/15
Comparing sequences without using alignments: application to HIV/SIV subtyping	13.5/15
Tractography Mapping for Dissimilarity Space across Subjects	14/15
Empirical Bayes method for reducing false discovery rates of correlation matrices with block diagonal structure	13.5/15